

Figure 1: MS alignment

1		60
E. coli MS	MTILNHTLGFPRVGLRRELKKAQESYWAGNSTREELLAVGRELRARHWDQQKQAGIDLLP	
yeast MS	MVQ.SAVLGFPRIGPNRELKKAQEGYWGKITYDELKFKVGDRLRTQNWKLQKEAGVDIIP	
tobacco MS	MA..SHIVGYPRMGPKRELKFALESFWDGKSSAEDLKVAADLRSSIWKQMAADAGIKYIP	
C. roseus MS	MA..SHIVGYPRMGPKRELKFALESFWDGKSSAEDLQKVAADLRSSIWKQMAADAGIKYIP	
corn MS/partial	
soy MS/partial	
61	120	
E. coli MS	VGDFAWYDHLVLTSLLLGNVPARHQN.KDGSVDIDTLFRIGRG..RAPTGE....PAAAA	
yeast MS	SNDFSFYDQVLDLSLLFNVIPDRYTKYDLSPY..DTLFAMGRGLQRKATETEKAVDVTAL	
tobacco MS	XNTFSYDQVLDLTTAMLGAVPARY.NWAGGEIAFDTYFSMARG.....NXSVPAM	
C. roseus MS	SNDFSYDQVLDLTTAMLGAVPPRY.NFAGGEIGFDTYFSMARG.....NASVPAM	
corn MS/partial	
soy MS/partial	
121	180	
E. coli MS	EMTKWFNTNYHYMVPEFVKQQFKLTWTQLLDEVDEALALGHKVKPVLGPTVTLWLKGV	
yeast MS	EMVKWFDSNYHYVRPTFSKTTQFKLNGQKPVDEFLEAKELGIHTRPVLGPTVSYLFLGKA	
tobacco MS	EMTKWXDNTNYHFI VPELGPDVNFYSYASHKAVDEYKEAKGLGVDTPVPLIGPVSYLLLSKP	
C. roseus MS	EMTKWFDTNYHYI VPELGPDVNFYSYASHKAVNEVYKEAKELGVDTPVPLVGPVTFLLLSKP	
corn MS/partial	
soy MS/partial	
181	240	
E. coli MS	.KGEQ..FDRLSLLNDILPVYQQVLAELAKRGIEWVQIDEPALVLELPQAWLDAKPAYD	
yeast MS	DKDSLDEPL.SLLEQLLPLYTEILSKLASAGATEVQIDEPVLVLDLPANAQAIAIKKAYT	
tobacco MS	AKGVEKSFPLLSLLDKVLPIYKEVIAELKAAGASWIQFDEPTLVLDLQAHQLEAFTKAYA	
C. roseus MS	AKGVEKTFPLLSLLDKILPVYKEVIGELKAAGASWIQFDEPTLVLDLQLEAFTKAYS	
corn MS/partial	
soy MS/partial	

FIGURE 1 CONTINUED

241
 E. coli MS
 yeast MS
 tobacco MS
 C. roseus MS
 corn MS/partial
 soy MS/partial
 300

241
 ALQGV...KLLLTTFEGVTPN...LDTITALPVQGLHVDLVHGKDDVAELHKRLPSD
 YFGEQSNLPKITLATYFGTVPN...LDAIKGLPVAALHVDVFVRAPEQFDEVVAAIGNK
 ELESSLSGLNVLTTETYFADVPAAEFKTLTALKG..VTAFGFDLVRGAQTLDLIKGGFPSPG
 ELESTLSGLNVI VETYFADIPAETYKILTALKG..VTGFGFDLVRGAKTLDLIKGGFPSPG

 301

WLLSAGLINGRNVWRADLTEKYAQIK...DIVGKRDLWVASSCSLLHSPIDL SVETRLDA
 QTL SVGI V DGRNIWK NDFKSSAIVNKAIEKLGADRVVATSSSLLHTPVDLNNETKLLDA
 KYLFAGVVDGRNIWANDLAASLNLQSLLEGIVGKDKLVVSTSCSLLHTAVDLVNETKLLDD
 KYLFAGVVDGRNIWANDLAASLSTLQSLLEGIVGKDKLVVSTSCSLLHTAVDLVNEPKLDDK

 361

E. coli MS
 yeast MS
 tobacco MS
 C. roseus MS
 corn MS/partial
 soy MS/partial
 420

EVKSWFAFALQCHELALLRDALNSGDTAA.LAEWSAPIQARRHSTRVHNPAVEKRLAAI
 EIKGFFSFATQKLDDEVVITKNVSGQDVAAALEANAKSVESRGKSKFIHDAAVKRRVASI
 EIKSWLAFAAQKVVEVNALAKALAXHKDEAFFSANATAQASRKSSPRVTNEAVQKAAAAL
 EIKSWLAFAAQKVVEVNALAKALAGEKDEAFFSENAAAQASRKSSPRVTNQAVQKAAAAL

 421

FAAQKVVEVNALAKALSGQKDEVFFSANAAALASRKSSPRVINEAVQKAAAAL
 480

TAQDSQRANVYEVRAEQARFKLPWPPTTTIGSFPPQTTEIRTLRLDFKKNLDANNYRT
 DEKMSTRAAPFEQRLPEQQKVFNLPLFPPTTTIGSFPPQTKDIRNRNKFNGKGTISAEEYEK
 KGSDHRRATNVSSRLDAQQKKNLNPVLPPTTTIGSFPPQTVELRRVRREYKAKKISEEEYVK
 RGSDHRRATTVSARLDAQQKKNLNPVLPPTTTIGSFPPQTLRLRRVRREYKAKKISEDDYVK

 KGSDHRRATNV SARLDAQQKKNLSVLPTTTIGSFPPQTADLRRVRREFKANKISEEEYVK
VTXGEXIS

FIGURE 1 CONTINUED

[illegible]

FIGURE 1 CONTINUED

780

721
NVPSVEWIEALLKKAARIIPAEERLWVNPDCGLKTRGWPETRAALANMVQAAQNLRG...
RIPSKDEFIAKISTILKSYPAEKFWVNPDCGLKTRGWEETRLSLTHMVEAAKYFREY..
RIPSTEEIADRVNKMMLAVLDTNIIWVNPDCGLKTRKYAEVVKPALENMVSAAKAIRTQLAS
RIPSTEEIADRINKMLAVLDTNIIWVNPDCGLKTRKYAEVVKPALENMVSAAKLIRTQLAS
.....
RIPPTEEIADRINKMLAVLEKNILWVNPDCGLKTRKYTEVKPALTNMVAACKLIRNELAK

E. coli MS
yeast MS
tobacco MS
C. roseus MS
corn MS/partial
soy MS/partial

781

E. coli MS ...
yeast MS KN.
tobacco MS SK.
C. roseus MS AK.
corn MS/partial ...

[illegible]

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*****
SEQ ID NO:02 MASHIVGYPRMGPVKRELKFALESFWDGKSSAEDLEKVAADLRSSIWKQMSAAGIKYIPSN *****
SEQ ID NO:04 MASHIVGYPRMGPVKRELKFALESFWDGKSSAEDLQKVAADLRSSIWKQMSAAGIKYIPSN *****
SEQ ID NO:06 MASHIVGYPRMGPVKRELKFALESFWDGKSSAEDLKKVAADLRSSIWKQMSAAGIKYIPSN *****
SEQ ID NO:08 MASHIVGYPRMGPVKRELKFALESFWDGKSSAEDLEKVAADLRSSIWKQMSAAGIKYIPSN *****
SEQ ID NO:10 -----
SEQ ID NO:11 MASHIVGYPRMGPVKRELKFALESFWDGKSSAEDLQKVAADLRSSIWKQMSAAGIKYIPSN *****
1
60

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[illegible]

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SEQ ID NO:02      ***** * ** * ** * ** * ** * ** *
VPELGPSTKFTYASHKAVSEYKEAKALGIDTVPVLVGPVSYLLSKPAKGVEKSFLLSL
SEQ ID NO:04      VPELGPDVNFTXASQKAVDEYKEAKALGVDTI PVLVGPVTYLLSKPAKGVEKSFLLSL
SEQ ID NO:06      VPELGPDVNFSYASHKAVDEYKEAKGLGVDTPVLIGPVSYLLSKPAKGVEKSFPLL
SEQ ID NO:08      VPEL-----
SEQ ID NO:10      -----
SEQ ID NO:11      VPELGPEVNFSYASHKAVNEYKEAKELGVDTPVLVGPVTFLLSKPAKGVEKTFPLL
121
180

```

[illegible]

SEQ ID NO:02	***** ** * * * * *	ETVFADIPAESYKTLTSLSGVTAYGFDLIRGAKTLDLRSSFPSGKYLFAGVVDGRNIWA
SEQ ID NO:04	***** ** * * * * *	ETVFADIPAEAYKTLTSLNGVTAYGFDLVRGTHLTDLIKGGFPSGKYLFAGVVDGRNIWA
SEQ ID NO:06	***** ** * * * * *	ETVFADVPAEAFKTLTALKGVTAFGFDLVRGAQTLDLIKGGFPSGKYLFAGVVDGRNIWA
SEQ ID NO:08	***** ** * * * * *	-----
SEQ ID NO:10	***** ** * * * * *	-----
SEQ ID NO:11	***** ** * * * * *	ETVFADIPAETYKIILTALKGVTFGFGLVRGAKTLDLIKGGFPSGKYLFAGVVDGRNIWA

241

300

[illegible]

FIGURE 2 CONTINUED

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***** * * * * * * * * * * * * * * * * * * * * * * * * * *
VNALAKALAGQKDEVYFAANAAQAARRSSPRVTNEEVQKAAALRGSDHRRSTTVSARL
VNALAKALSGNKDVAFFSANAAQAARRSSPRVTNEAVQKAAALRGSDHRRATNV SARL
VNALAKALAGHKDEAFFSANATAQAARRSSPRVTNEAVQKAAALRGSDHRRATNVSSRL
-----
-----SSPRVNNE-VQKAAALRGSDHRRATPVSARL
VNALAKALAGEKDEAFFSENAAQAARRSSPRVTNQAVQKAAALRGSDHRRATTVSARL
361 420

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SEQ ID NO:02
SEQ ID NO:04
SEQ ID NO:06
SEQ ID NO:08
SEQ ID NO:10
SEQ ID NO:11

```

```

***** * * * * * * * * * * * * * * * * * * * * * * * * * *
DAQQKKLNLPLPTTTIGSFQTVELRRVRREYKAKKITEDEYISAIKEEISKVVVKIQEE
DAQQKKLNLPLPTTTIGSFQTVELRRVRREYKAKKISEEYVKSIIKEEIRKVVVELQEE
DAQQKKLNLPLPTTTIGSFQTVELRRVRREYKAKKISEEYVKAIEIKKVVDLQEE
-----
DAQQKKLNLPLPTTTIGSFQTMDLRRVRREYKAKEDLGVCQCYQGRNXQRLSRFKEE
DAQQKKLNLPLPTTTIGSFQTVLELRRVRREYKAKKISEDDYVKAIEEISKVVVKLQEE
421 480

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SEQ ID NO:02
SEQ ID NO:04
SEQ ID NO:06
SEQ ID NO:08
SEQ ID NO:10
SEQ ID NO:11

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***** * * * * * * * * * * * * * * * * * * * * * * * * * *
LDIDVLVHGEPERNDMVEYFGEQLSGFAFTANGWVQSYGSRVCVKPPIIYGDVSRPNPMTV
LDIDVLVHGEPERNDMVEYFGEQLSGFAFTANGWVQSYGSRVCVKPPIIYGDVSRPKPMTV
LDIDVLVHGEPERNDMVEYFGEQLSGFAFTANGWVQSYGSRVCVKPPIIYGDVSRPNPMTV
-----
LDIDVLXQ-----
LDIDVLVHGEPERNDMVEYFGEQLSGFAFTANGWVQSYGSRVCVKPPIIYGDVSRPNPMTV
481 540

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SEQ ID NO:02
SEQ ID NO:04
SEQ ID NO:06
SEQ ID NO:08
SEQ ID NO:10
SEQ ID NO:11

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[Faint, illegible markings]

SEQ ID NO:02
SEQ ID NO:04
SEQ ID NO:06
SEQ ID NO:08
SEQ ID NO:10
SEQ ID NO:11

SEQ	ID	NO:02
SEQ	ID	NO:04
SEQ	ID	NO:06
SEQ	ID	NO:08
SEQ	ID	NO:10
SEQ	ID	NO:11

SEQ	ID	NO:02
SEQ	ID	NO:04
SEQ	ID	NO:06
SEQ	ID	NO:08
SEQ	ID	NO:10
SEQ	ID	NO:11

SEQ	ID	NO:02
SEQ	ID	NO:04
SEQ	ID	NO:06
SEQ	ID	NO:08
SEQ	ID	NO:10
SEQ	ID	NO:11

* * * * * VFDTNILWVNPDCGLKTRKYTEVKPALTNMVSATKLIRQLASAK
* * * * * VLEKNILWVNPDCGLKTRKYTEVKPPSQNMVAAKLIYELA--K
* * * * * VLDTNILWVNPDCGLKTRKYAEVKPALENMVSAAKAIRQLASSK
* * * * * -----
* * * * * -----
* * * * * VLDTNILWVNPDCGLKTRKYAEVKPALENMVSAAKLIRQLASAK
* * * * * 721 765

721